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<110> Bristol-Myers Squibb Company
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RECEIVED

JUL 29 2002

TECH CENTER 1600/2900

INS
D2
CT

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C1

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 Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile Pro Ala Gly
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 Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu
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 Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu
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 Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg
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 Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val
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 Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
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 Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro
 245 250 255
 Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu
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 Asp Asn Gly Tyr Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu
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 His Leu Pro Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln
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 Cys Gln Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro
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C1

Pro Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
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 Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr
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 Arg Thr Asp Leu Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro
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 Arg Tyr Thr Gly Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln
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 Gly Thr Pro Cys Ser Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg
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Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe
785 790 795 800

Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp
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C1

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Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln	
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Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser	
420 425 430	
aca gaa gat aag cgc tta atg tct tcc atc ctt acc agc att gat gca	1464
Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala	
435 440 445	
tct aag ccc tgg tcc aaa tgc act tca gcc acc atc aca gaa ttc ctg	1512
Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu	
450 455 460	
gat gat ggc cat ggt aac tgt ttg ctg gac cta cca cga aag cag atc	1560
Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile	
465 470 475 480	
ctg ggc ccc gaa gaa ctc cca gga cag acc tac gat gcc acc cag cag	1608

C

Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln
 485 490 495
 tgc aac ctg aca ttc ggg cct gag tac tcc gtg tgt ccc ggc atg gat 1656
 Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp
 500 505 510
 gtc tgt gct cgc ctg tgg tgt gct gtg gta cgc cag ggc cag atg gtc 1704
 Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val
 515 520 525
 tgt ctg acc aag aag ctg cct gcg gtg gaa ggg acg cct tgt gga aag 1752
 Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys
 530 535 540
 ggg aga atc tgc ctg cag ggc aaa tgt gtg gac aaa acc aag aaa aaa 1800
 Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys
 545 550 555 560
 tat tat tca acg tca agc cat ggc aac tgg gga tct tgg gga tcc tgg 1848
 Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp
 565 570 575
 ggc cag tgt tct cgc tca tgt gga gga gga gtg cag ttt gcc tat cgt 1896
 Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg
 580 585 590
 cac tgt aat aac cct gct ccc aga aac aac gga cgc tac tgc aca ggg 1944
 His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly
 595 600 605
 aag agg gcc atc tac cgc tcc tgc agt ctc atg ccc tgc cca ccc aat 1992
 Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn
 610 615 620
 ggt aaa tca ttt cgt cat gaa cag tgt gag gcc aaa aat ggc tat cag 2040
 Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln
 625 630 635 640
 tct gat gca aaa gga gtc aaa act ttt gtg gaa tgg gtt ccc aaa tat 2088
 Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr
 645 650 655
 gca ggt gtc ctg cca gcg gat gtg tgc aag ctg acc tgc aga gcc aag 2136
 Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys
 660 665 670
 ggc act ggc tac tat gtg gta ttt tct cca aag gtg acc gat ggc act 2184
 Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr
 675 680 685
 gaa tgt agg ccg tac agt aat tcc gtc tgc gtc cgg ggg aag tgt gtg 2232
 Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val
 690 695 700
 aga act ggc tgt gac ggc atc att ggc tca aag ctg cag tat gac aag 2280
 Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys

705	710	715	720	
tgc gga gta tgt gga gga gac aac tcc agc tgt aca aag att gtt gga				2328
Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly	725	730	735	
acc ttt aat aag aaa agt aag ggt tac act gac gtg gtg agg att cct				2376
Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro	740	745	750	
gaa ggg gca acc cac ata aaa gtt cga cag ttc aaa gcc aaa gac cag				2424
Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln	755	760	765	
act aga ttc act gcc tat tta gcc ctg aaa aag aaa aac ggt gag tac				2472
Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr	770	775	780	
ctt atc aat gga aag tac atg atc tcc act tca gag act atc att gac				2520
Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp	785	790	795	800
atc aat gga aca gtc atg aac tat agc ggt tgg agc cac agg gat gac				2568
Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp	805	810	815	
ttc ctg cat ggc atg ggc tac tct gcc acg aag gaa att cta ata gtg				2616
Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val	820	825	830	
cag att ctt gca aca gac ccc act aaa cca tta gat gtc cgt tat agc				2664
Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser	835	840	845	
ttt ttt gtt ccc aag aag tcc act cca aaa gta aac tct gtc act agt				2712
Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser	850	855	860	
cat ggc agc aat aaa gtg gga tca cac act tcg cag ccg cag tgg gtc				2760
His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val	865	870	875	880
acg ggc cca tgg ctc gcc tgc tct agg acc tgt gac aca ggt tgg cac				2808
Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His	885	890	895	
acc aga acg gtg cag tgc cag gat gga aac cgg aag tta gca aaa gga				2856
Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly	900	905	910	
tgt cct ctc tcc caa agg cct tct gcg ttt aag caa tgc ttg ttg aag				2904
Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys	915	920	925	
aaa tgt tagcctgtgg ttatgatctt atgcacaaag ataactggag gattcagcac				2960
Lys Cys	930			

C1

cgatgcagtc gtggtgaaca ggaggtctac ctaacgcaca gaaagtcattg cttcagtgac 3020
 attgtcaaca ggagtccaat tatgggcaga atctgctctc tgtgaccaa agaggatgtg 3080
 cactgcttca cgtgacagtg gtgaccttgc aatatagaaa aacttgggag ttattgaaca 3140
 tcccttggga ttacaagaaa cactgatgaa tggttaaata ggggacattt gaagatggca 3200
 gaactgtctc ccccttgtca cctacctctg aatagaatgt ctttaatggt 3250

<210> 15

<211> 930

<212> PRT

<213> Homo sapiens

<400> 15

Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro
 1 5 10 15

Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly
 20 25 30

Gln Pro Pro Thr Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly
 35 40 45

Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu
 50 55 60

Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu
 65 70 75 80

Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg
 85 90 95

Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly
 100 105 110

Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser
 115 120 125

His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala
 130 135 140

Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His
 145 150 155 160

Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu
 165 170 175

Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val
 180 185 190

C1

Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser
 195 200 205
 Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala
 210 215 220
 His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp
 225 230 235 240
 Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp
 245 250 255
 Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu
 260 265 270
 Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln
 275 280 285
 His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His
 290 295 300
 Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val
 305 310 315 320
 Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr
 325 330 335
 Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly
 340 345 350
 Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu
 355 360 365
 Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val
 370 375 380
 Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp
 385 390 395 400
 Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu
 405 410 415
 Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser
 420 425 430
 Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala
 435 440 445
 Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu
 450 455 460
 Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile
 465 470 475 480
 Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln
 485 490 495

Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp
 500 505 510
 Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val
 515 520 525
 Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys
 530 535 540
 Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys
 545 550 555 560
 Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp
 565 570 575
 Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg
 580 585 590
 His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly
 595 600 605
 Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn
 610 615 620
 Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln
 625 630 635 640
 Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr
 645 650 655
 Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys
 660 665 670
 Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr
 675 680 685
 Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val
 690 695 700
 Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys
 705 710 715 720
 Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly
 725 730 735
 Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro
 740 745 750
 Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln
 755 760 765
 Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr
 770 775 780
 Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp
 785 790 795 800

C1

Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp
805 810 815

Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val
820 825 830

Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser
835 840 845

Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser
850 855 860

His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val
865 870 875 880

Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His
885 890 895

Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly
900 905 910

Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys
915 920 925

Lys Cys
930

<210> 16

<211> 42

<212> PRT

<213> Homo sapiens

<400> 16

Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Leu Val Ala Asp Ala
1 5 10 15

Ser Met Ala Arg Met Tyr Gly Arg Gly Leu Gln His Tyr Leu Leu Thr
20 25 30

Leu Ala Ser Ile Ala Asn Lys Leu Tyr Phe
35 40

<210> 17

<211> 23

<212> DNA

<213> Mus musculus

<400> 17

cggccacgac cctcaagaac ttt

<210> 18

<211> 25

<212> DNA

<213> Mus musculus

<400> 18

gcatggaggc catcatcttc aatca

25

<210> 19

<211> 22

<212> DNA

<213> Homo sapiens

<400> 19

gggaggattt atgtgggcat ca

22

<210> 20

<211> 23

<212> DNA

<213> Homo sapiens

<400> 20

gtgcatttgg accagggctt aga

23

<210> 21

<211> 13

<212> PRT

<213> artificial

<220>

<223> Synthesized peptide.

<220>

<221> MOD_RES

<222> (12)..(12)

<223> Acp

<400> 21

Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Xaa Cys

1

5

(-20)

C1